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GenCore version 5.1.3  
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OM protein - protein search, using sw model

Run on: November 9, 2002, 04:28:16 : Search time 49 Seconds

(without alignments)  
372.766 Million cell updates/sec

Title: US-09-895-298A-83

Sequence: 1 MNFQPPSKAMRASQMMTFP.....HDSLDLRSRVQEGNPRA 190

Scoring table:

BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283224 seqs, 96134422 residues

Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 45 summaries

Database :

PIR-73:\*  
1: pirl:\*  
2: pirl:\*  
3: pirl:\*  
4: pirl:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query	Match Length	DB ID	Description
1	99.5	9.9	1203	2	H89606
2	94.5	9.4	451	2	A96920
3	88	8.8	322	2	C70905
4	87.5	8.7	261	2	T20264
5	87	8.7	272	2	H83535
6	84.5	8.4	713	2	H83684
7	84	8.4	399	2	D70072
8	81.5	8.1	154	2	AD1677
9	81.5	8.1	261	2	AH2288
10	80.5	8.0	200	2	G83834
11	80	8.0	378	2	S61981
12	80	8.0	443	2	B26596
13	79.5	7.9	154	2	AD1305
14	79.5	7.9	217	2	AC2538
15	79.5	7.9	396	2	H89869
16	79.5	7.9	772	2	E96977
17	79	7.9	239	2	AD0593
18	78.5	7.8	229	2	G90027
19	78	7.8	319	2	T21402
20	77.5	7.7	306	2	D71609
21	77.5	7.7	515	2	AF2321
22	77.5	7.7	604	2	G89864
23	77	7.7	288	2	A39956
24	77	7.7	342	2	A38908
25	77	7.7	392	2	F84566
26	77	7.7	564	2	F90965
27	77	7.7	564	2	F85813
28	77	7.7	605	2	H71562
29	76.5	7.6	176	2	AD0072

30	76.5	7.6	322	2	D37753	Pnc protein - Sal
31	76	7.6	447	2	D81336	probable K+ uptake
32	76	7.6	589	2	H64959	probable membrane
33	76	7.6	661	2	T47467	hypothetical prote
34	75.5	7.5	703	2	T24975	hypothetical prote
35	75.5	7.5	975	2	T16073	hypothetical prote
36	75.5	7.5	1695	2	J60084	voltage-gated sodi
37	75.5	7.5	1695	2	J60084	cell wall alpha-gl
38	75	7.5	175	2	T43731	hypothetical prote
39	75	7.5	209	2	H71896	hypothetical prote
40	75	7.5	445	2	E22845	hypothetical prote
41	75	7.5	1053	2	S58883	calcium channel no
42	74.5	7.4	148	1	T12787	probable protein-d
43	74.5	7.4	267	2	A82997	hypothetical prote
44	74.5	7.4	308	2	H68268	hypothetical prote
45	74.5	7.4	348	2	AE0049	M48 peptidase fam1

#### ALIGNMENTS

##### RESULT 1

H89606

protein B0416.1 [imported] - Caenorhabditis elegans

C:Species: Caenorhabditis elegans

C:Date: 10-May-2001 #sequence\_revision 10-May-2001 #text\_change 09-Nov-2001

C:Accession: H89606

R:Anonymous, The C. elegans Sequencing Consortium.

Science 282, 2012-2018, 1998

A:Title: Genome sequence of the nematode C. elegans: a platform for investigating bio

A:Reference number: A75000; MUID:99069613; PMID:9851916

A:Note: see websites genome.wustl.edu/gsc/C.elegans/ and www.sanger.ac.uk/Projects/C-

A:Note: published errata appeared in Science 283, 35, 1999; Science 283, 2103, 1999;

A:Accession: H89606

A>Status: preliminary

A:Molecule type: DNA

A:Residues: 1-1203 <STO>

A:Cross-references: GB:chr\_X; PIDN:AAB36841.2; PID:g4850180; GSPDB:GNO0028; CESP:B041

A:Gene: B0416.1

A:Map position: X

Query Match

Best Local Similarity 9.9%; Score 99.5; DB 2; Length 1203;

Matches 39; Conservative 23; Mismatches 50; Indels 29; Gaps 8;

QY 6 PPSKAMRASQMMFFFLFPSPFTGLCTLAIT-TIMRLKPSADGCPRLPFTHSY 63

DB 701 PASQIFRASRSNFFALLILFLF--LCTLPVGFVIASKTPSKSCGP-GMOSFFYSVI 756

QY 64 SWIDTSTREGYLWVWYINRLGSHVFF-----ILTVLITTYLYWOIT---EG 112

DB 757 T--DVLEN-----LDDTLVNGIKYSLSPGIIPVLVLSIVYFLIAVATGSLQAN 806

QY 113 KTIMRLHGOINEGRDKMF 133

DB 807 QDLSFOLWVER--TEKKKIF 825

##### RESULT 2

A96920

Probable ABC transporter, permease component CAC0165 [imported] - Clostridium acetobu

C:Species: Clostridium acetobutylicum

C:Date: 14-Sep-2001 #sequence\_revision 14-Sep-2001 #text\_change 14-Sep-2001

C:Accession: A96920

R:Moiling, J.; Breton, G.; Omeichenko, M.V.; Markarova, K.S.; Zeng, Q.; Gibson, R.; L

J. Bacteriol. 183, 4823-4838, 2001

A:Title: Genome Sequence and Comparative Analysis of the Solvent-Producing Bacterium

A:Reference number: A96900; MUID:21359325; PMID:21359325

A:Accession: A96920

A>Status: preliminary

A:Molecule type: DNA

A:Residues: 1-451 <KUR>  
 A:Cross-references: GB:AE001437; PIDN:AAK78148.1; PID:915022994; GSPDB:GN00168  
 A:Experimental source: Clostridium acetobutylicum ATCC824  
 C:Genetics:  
 A:Gene: CAC0165

Query Match 9.4%; Score 94.5; DB 2; Length 451;  
 Best Local Similarity 24.8%; Pred. No. 0.44; Mismatches 53; Indels 21; Gaps 6;  
 Matches 35; Conservative 32; Mismatches 53; Indels 21; Gaps 6;  
 DB 23 LFFPSTGVLTCTAATITRLKPSADCGPFRGLPLFIHSISWIDTSTRPGYLWVWI 81  
 104 LLEQNALIEITIGCALGILIGML-----MPFIISIMY-----TIGKTKGLWVLSN 149  
 QY 82 YRNIGSVHEFFITLVLITLYLWQITGKIMIRLHEQINSGKDKMFL-TEKLIK 140  
 DB 150 Y-SIGGTIALIFOLVYVITGDSYSTSTRE---VIDLSEKSRPKKRYLSTAEITE 204  
 QY 141 LQMEKKANPSLVLEEREVE 161  
 DB 205 IIGKKKTSHTKIKILNEDID 225

## RESULT 3

C70905  
 hypothetical protein RV0176 - Mycobacterium tuberculosis (strain H37RV)

C:Species: Mycobacterium tuberculosis  
 C:Date: 17-Jul-1998 #sequence\_revision 17-Jul-1998 #text\_change 20-Jun-2000  
 C:Accession: C70905  
 R:Coile, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, S.; Connor, R.; Davies, R.; Devlin, K.; Feltham, T.; Gentles, S.; Hamlin, N.; Holroyd, S.; Rajandram, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S. Nature 393, 537-544, 1998  
 A:Authors: Squares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.  
 A:Title: Deciphering the biology of Mycobacterium tuberculosis from the complete genome  
 A:Reference number: A70500; MUID:98295987; PMID:9634230  
 A:Accession: C70905  
 A:Status: preliminary; nucleic acid sequence not shown; translation not shown  
 A:Molecule type: DNA  
 A:Residues: 1-322 <COL>  
 A:Cross-references: GB:Z97050; GB:ML123456; NID:93256008; PIDN:CAB09743.1; PID:92213513  
 A:Experimental source: strain H37RV  
 C:Genetics:  
 A:Gene: RV0176  
 C:Superfamily: Mycobacterium tuberculosis hypothetical protein RV0176

Query Match 8.8%; Score 88; DB 2; Length 322;  
 Best Local Similarity 31.0%; Pred. No. 1.2; Mismatches 32; Indels 12; Gaps 4;  
 Matches 26; Conservative 14; Mismatches 32; Indels 12; Gaps 4;  
 QY 6 PPSKAMR-ASOMMTFFIL-----LFFPSTGVLTCTAATITWRL--KPSADCGPFRGLP 56  
 DB 52 PPSANRWLCAACILGLTILLAVNRLLFTITGMSLGRALGIRVYRRDGSALGWR--- 108  
 QY 57 LFHSISWIDTSTRPGYLWVWI 80  
 DB 109 LLYVRLAHLYDTLSLFGWMLPLM 132

## RESULT 4

T20264  
 hypothetical protein C56A3.4 - Caenorhabditis elegans

C:Species: Caenorhabditis elegans  
 C:Date: 15-Oct-1999 #sequence\_revision 15-Oct-1999 #text\_change 15-Oct-1999  
 C:Accession: T20264  
 R:Sims, M.  
 submitted to the EMBL Data Library, July 1996  
 A:Reference number: Z19244  
 A:Accession: T20264  
 A:Status: preliminary; translated from GB/EMBL/DBJ  
 A:Molecule type: DNA  
 A:Residues: 1-261 <ML>  
 A:Cross-references: EMBL:Z77655; PIDN:CAB01133.1; GSPDB:GN00023; CESP:C56A3.4

A:Experimental source: clone C56A3  
 C:Genetics:  
 A:Gene: CESP:C56A3.4  
 A:Map position: 5  
 A:Introns: 107/3; 135/2; 157/2; 218/3

Query Match 8.7%; Score 87.5; DB 2; Length 261;  
 Best Local Similarity 23.3%; Pred. No. 1.1; Mismatches 44; Indels 27; Gaps 4;  
 Matches 30; Conservative 28; Mismatches 44; Indels 27; Gaps 4;  
 QY 5 QPSKAMRASOMMTFFILFFPSTGVLTCTAATITWRLKPSADCGPFRGLPLFIH-SIY 63  
 DB 7 EEPDQALQASRTAFDYLFKLFYPPYFFVTLPIRITWTF-----FTNPFVSSLSLF 57  
 QY 64 SWIDTSTRPGYLWVWIYRNIGSVHFFI-----LTLIILITLYLWQITEG 112  
 DB 58 LFIATV-----LTLIVYRRLSTPRESTISYITLVYGVSIYTVGFIFFPVRIV 111  
 QY 113 RKIMIRLH 121  
 DB 112 TRIIDVLH 120

## RESULT 5

H85355  
 senescence-associated protein homolog [imported] - Arabidopsis thaliana

C:Species: Arabidopsis thaliana (mouse-ear cress)  
 C:Date: 16-Feb-2001 #sequence\_revision 16-Feb-2001 #text\_change 02-Mar-2001  
 C:Accession: H85355  
 R:Ranby, M.; The European Union Arabidopsis Genome Sequencing Consortium, The Cold SP  
 Nature 402, 769-777, 1999  
 A:Title: Sequence and analysis of chromosome 4 of the plant Arabidopsis thaliana.  
 A:Reference number: A85001; MUID:20083488; PMID:10617198  
 A:Accession: H85355  
 A:Status: preliminary  
 A:Molecule type: DNA  
 A:Residues: 1-272 <STO>  
 A:Cross-references: GB:NC\_001268; NID:97269944; PIDN:CAB79761.1; GSPDB:GN00140  
 A:Map position: 4  
 C:Superfamily: Arabidopsis thaliana hypothetical protein F9K21.180

Query Match 8.7%; Score 87; DB 2; Length 272;  
 Best Local Similarity 27.0%; Pred. No. 1.2; Mismatches 40; Indels 18; Gaps 4;  
 Matches 27; Conservative 15; Mismatches 40; Indels 18; Gaps 4;  
 QY 16 MMTFFILFFPSTGVLTCTAATITWRLKPSADCGPFRGLPLFIHSISWIDTSTRPG 74  
 DB 11 IIMFFVLLSV-----ILSTGIMLSKATQOCERFLDKPMIALGVFLMILTAAGVG 63  
 QY 75 ----YIMVWVYRNIGSVHFFITLVLITLYLWQITEG 110  
 DB 64 SCRRVTLIMSY-----LFVMPFLILVLCFTTFEAVVT 97

## RESULT 6

H83684  
 hypothetical protein BH0280 [imported] - Bacillus halodurans (strain C-125)

C:Species: Bacillus halodurans  
 C:Date: 01-Dec-2000 #sequence\_revision 01-Dec-2000 #text\_change 15-Jun-2001  
 C:Accession: H83684  
 R:Takaki, H.; Nakasone, K.; Takaki, Y.; Maeno, G.; Sasaki, R.; Masui, N.; Fujii, F.; H  
 Nucleic Acids Res. 28, 4317-4331, 2000  
 A:Title: Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans a  
 A:Reference number: A83650; MUID:20512582; PMID:11058132  
 A:Accession: H83684  
 A:Status: preliminary  
 A:Molecule type: DNA  
 A:Residues: 1-713 <STO>  
 A:Cross-references: GB:AP001508; GB:BA000004; NID:910172890; PIDN:BAB03999.1; GSPDB:G  
 A:Experimental source: strain C-125  
 C:Genetics:

A:Gene: BH0280

Query Match 8.4%; Score 84.5; DB 2; Length 713;

Best Local Similarity 21.7%; Pred. No. 6.3; Mismatches 58; Indels 89; Gaps 11;

Matches 47; Conservative 23; Mismatches 58; Indels 89; Gaps 11;

QY 6 PPSKAMR-----ASQMPFFI-----FLFPSPFVGLCTLATIYMLKPSA 47  
 DB 194 PRTLAWLMTGLMLMYIRNGKTAIYSHGFSLF-----KIMRRLLGN 240  
 QY 48 DCGPRG-----LPLFIHSYMWIDLTSTRGYLMVWVYIRNLISGSHFFLLIYLI 102  
 DB 241 ACVVFAVYLLPLLAFLAFGWM-----OPRYLFAAMV-----TGSWPELLLAISFLF 290  
 QY 103 TYLWQIIEGRKIMRLHEQIINEGKDKMFLIEK-----LTKLOD-----M 144  
 DB 291 FY-----SSRSSLI-----ESKNTKTKLFLITSQVAKVVALSVIVLQIADRLTIM 340  
 QY 145 EKKAN-----PSSLVLREREEVQCGFL 166  
 DB 341 EEVRSMTDMAFGKDYGFEPHSIGYDQEMNGESGL 377

## RESULT 7

D70072

antibiotic resistance protein homolog yxam - Bacillus subtilis

C:Species: Bacillus subtilis

C:Date: 05-Dec-1997 #sequence\_revision 05-Dec-1997 #text\_change 15-Oct-1999

C:Accession: D70072

R:Kunzt, F.; Ogawara, N.; Moszer, I.; Albertini, A.M.; Alloni, G.; Azevedo, V.; Berter

A.; Bron, S.; Broillett, S.; Brusch, C.V.; Caldwell, B.; Capiano, V.; Carter, N.M.; Chd

A.; Ehrlich, S.D.; Emerson, P.T.; Entian, K.D.; Errington, J.; Fabret, C.; Ferrati, E.

Nature 390, 249-256, 1997

A:Authors: Foulger, D.; Fritz, C.; Fujita, M.; Fujita, Y.; Fuma, S.; Galizeli, A.; Gall

leach, J.; Harwood, C.R.; Henuat, A.; Hilbert, H.; Holsappel, S.; Hosono, S.; Hullo, M.F.

Koelter, P.; Konigstein, G.; Krogh, S.; Kumano, M.; Kurita, K.; Lapidus, A.; Lardinois,

A:Authors: Lauber, J.; Lazarevic, V.; Lee, S.M.; Levine, A.; Liu, H.; Masuda, S.; Maueel

Y, M.; Ogawa, K.; Ogilawa, A.; Oudega, B.; Park, S.H.; Parro, V.; Pohl, T.M.; Portetelle

Rieger, M.; Rivolta, C.; Rocha, E.; Roche, B.; Rose, M.; Sadale, Y.; Sato, T.; Scanlon,

A:Authors: Schleich, S.; Schroeter, R.; Scoffone, F.; Sekiguchi, J.; Sekowska, A.; Setor

akuech, M.; Tamakoshi, A.; Tanaka, T.; Terpiltra, P.; Tognoni, A.; Tosato, V.; Uchiyama,

T.; Winters, P.; Wipac, A.; Yamamoto, H.; Yamane, K.; Yasunori, K.; Yata, K.; Yoshida, K

A:Authors: Yoshikawa, H.F.; Zumbstein, E.; Yoshikawa, H.; Dancin, A.

A:Title: The complete genome sequence of the Gram-positive bacterium Bacillus subtilis.

A:Reference number: A69580; MUID:98044033; PMID:9384377

A:Accession: D70072

A:Status: preliminary; nucleic acid sequence not shown; translation not shown

A:Molecule type: DNA

A:Residues: 1-399 &lt;KUN&gt;

A:Cross-references: GB:299124; GB:AL009126; NID:g2636442; PIDN:CAB16029.1; PID:ell184718;

A:Experimental source: strain 168

C:Genetics:

A:Gene: yxam

Query Match 8.4%; Score 84; DB 2; Length 399;

Best Local Similarity 19.9%; Pred. No. 3.6; Mismatches 48; Indels 62; Gaps 8;

Matches 35; Conservative 31; Mismatches 48; Indels 62; Gaps 8;

QY 4 TQPSKAMR-----RASQMPFFIPL--FFPSF-TGVLCYLAITWMLKPSADCGPR 53  
 DB 50 FEPVSGVADRYGKISSTFFSILTWAFPFIDSAICILAMILWLSLSGSPE 109  
 QY 54 GLPLFIHSYMWIDLTSTRGYLMVWVYIRNLISG 89  
 DB 110 -----TWMSRVAGDRFGKEMKNTQLLITFLIGSISAGSLVSLNLY----- 152  
 QY 90 HFFFLITLIVLITLYWQITEGRKIMRLHEQIINEG-----KQKMFIEKLIK 141  
 DB 153 -FPFLVAVIYLLFIW-----MSYFIKVPVSSETNHGDQNHQSIKIKESLKI 201

## RESULT 8

AD1677

signal peptidase II homolog lsp [imported] - Listeria innocua (strain C1p11262)

C:Species: Listeria innocua

C:Date: 27-Nov-2001 #sequence\_revision 27-Nov-2001 #text\_change 14-Dec-2001

C:Accession: AD1677

R:Glaser, P.; Franke, U.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Bloec

D.; Dominguez-Bernal, G.; Duchaud, E.; Durand, L.; Dussurge, O.; Entian, K.D.; Fsihl,

Science 294, 849-852, 2001

A:Authors: Kreft, J.; Kuhn, M.; Kunst, F.; Kurapat, G.; Madueno, E.; Maitournam, A.;

Ok, C.; Schluter, T.; Simoes, N.; Tiller, A.; Vazquez-Boland, J.A.; Voss, H.; Wehla

A:Title: Comparative genomics of Listeria species.

A:Reference number: AB1077; MUID:21537279; PMID:11679669

A:Accession: AD1677

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-154 &lt;GLA&gt;

A:Cross-references: GB:AL592022; PIDN:CAC97188.1; PID:916414459; GSPDB:GN00178

A:Experimental source: strain C1p11262

C:Genetics:

A:Gene: lsp

C:Superfamily: lipoprotein signal peptidase

Query Match 8.1%; Score 81.5; DB 2; Length 154;

Best Local Similarity 22.4%; Pred. No. 2.1; Mismatches 22; Indels 49; Gaps 7;

Matches 28; Conservative 26; Mismatches 22; Indels 49; Gaps 7;

QY 33 ICTLAI-----TMRKPSADCGPRGLPFIHSYMWIDLTSTRGYLMVWVYIRN 84  
 DB 5 LITLVAIVALDQITKWIYVONMEIG-----QKIEVIGPLY--WTSYRND 46  
 QY 85 -----LIGSVHFFLLFVLI--ITLYWQITEGRKI-----MIRLIL 121  
 DB 47 GAMSILBCHMFFLYIYVIGIITIMQKAKKRFLFSISLAFILGGAIGNFDRILH 106  
 QY 122 EQIIN 126  
 DB 107 QEVVD 111

## RESULT 9

AH2288

hypothetical protein alr3863 [imported] - Nostoc sp. (strain PCC 7120)

C:Species: Nostoc sp.

A:Note: Nostoc sp. strain PCC 7120 is a synonym of Anabaena sp. strain PCC 7120

C:Date: 14-Dec-2001 #sequence\_revision 14-Dec-2001 #text\_change 30-Jun-2002

C:Accession: AH2288

R:Kaneko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Itigu

Nakazaki, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata

DNA Res. 8, 205-213, 2001

A:Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium

A:Reference number: AB1807; MUID:21595285; PMID:11759840

A:Accession: AH2288

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-261 &lt;KUN&gt;

A:Cross-references: GB:BA000019; PIDN:BA075562.1; PID:gl7132997; GSPDB:GN00179

A:Experimental source: strain PCC 7120

C:Genetics:

A:Gene: alr3863

Query Match 8.1%; Score 81.5; DB 2; Length 261;

Best Local Similarity 19.4%; Pred. No. 3.9; Mismatches 70; Indels 81; Gaps 9;

Matches 46; Conservative 40; Mismatches 70; Indels 81; Gaps 9;

QY 29 FTGVLC-----TLATITWRLKPSADCGPRGLPFIHS 61  
 DB 13 FGVICDGLIEFEVAMRTYQIWSPAENTPPDIALRFRRLRPVLETG--WEMPVLAKA 70  
 QY 62 -----ITSWD-----TLSTRGYLMVWVYIRNLIG--SVHFF-- 93  
 DB 71 IVDGNSDDQIIOBWTSTPKILLDDKLAQKELATKIDGIRDEMIANDLGDWLSLHREYOG 130  
 QY 94 ---ILTLVILITLYWQITEGRKIMIRLHEQIINEGDKMF-----LIEKLIK 140

Db 131 VIKRLKINAVSEVKLIYVTTKEGRVEQQLHOGSDVDPRAITGKEYKRPKEITIRLIQ 190  
QY 141 LOD-----MEKKANPSSVLEREVEQOQGLHLGEHGDSDLRSRSGVGNPR 189  
Db 191 AADHEPVSLSMFVEDRIKTQLVQOQSDLED---VKFLMDMGVINTQSERKAASDPR 244  
RESULT 10  
G83834  
hypothetical protein BH1479 [imported] - Bacillus halodurans (strain C-125)  
C:Species: Bacillus halodurans  
C:Date: 01-Dec-2000 #sequence\_revision 01-Dec-2000 #text\_change 15-Jun-2001  
C:Accession: G83834  
R:Takami, H.; Nakasone, K.; Takaki, Y.; Maeno, G.; Sasaki, R.; Masui, N.; Fujii, F.; Hara  
Nucleic Acids Res. 28, 4317-4331, 2000  
A:Title: Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans and  
A:Reference number: A83650; MUID:20512582; PMID:11058132  
A:Accession: G83834  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-200 <STO>  
A:Cross-references: GB:AP001512; GB:BA000004; NID:g10174030; PIDN:BA05198.1; GSPDB:GN00  
A:Experimental source: strain C-125  
C:Genetics:  
A:Gene: BH1479  
Query Match 8.0%; Score 80.5; DB 2; Length 200;  
Best Local Similarity 23.8%; Pred. No. 3.5;  
Matches 36; Conservative 25; Mismatches 55; Indels 35; Gaps 6;  
QY 19 FFLLFFPSFTG-----VICTLA-----ITWRKPSADCGPRGLPRT 59  
Db 10 FFALLLMTFSQWQPLDFWIPDISLVSALIFPSRPIKRRKPLTGLSL 69  
QY 60 HSYS---NIDLTSTPRGYLWVYIRNLGSGVFFFLTLVLIIT--TYLW----- 107  
Db 70 YGLFAFGKMLITITGPIPLASLETLY-DMIRPEWMAHYFLVFIITGDELFWRGVVGT 128  
QY 108 ---QITGRKIMIRLHEQIINEGDKMFLI 135  
Db 129 LHMQSEGRLITFGALLGYVHAASSLLLV 159  
RESULT 11  
S61981  
probable membrane protein YOL003c - Yeast (Saccharomyces cerevisiae)  
N:Alternate names: hypothetical protein O2389; hypothetical protein UNE378  
C:Species: Saccharomyces cerevisiae  
C:Date: 10-Apr-1996 #sequence\_revision 19-Apr-1996 #text\_change 19-Apr-2002  
C:Accession: S61981; S66884; S66885; S72130  
R:Starky, F.; Uhlen, M.  
submitted to the EMBL Data Library, December 1995  
A:Reference number: S61981  
A:Accession: S61981  
A:Molecule type: DNA  
A:Residues: 1-378 <STB>  
A:Cross-references: EMBL:U43491; NID:g1150992; PID:g1150993  
R:Petersson, B.; Starky, F.; Uhlen, M.  
submitted to the Protein Sequence Database, July 1996  
A:Reference number: S66882  
A:Accession: S66884  
A:Molecule type: DNA  
A:Residues: 1-378 <PBT>  
A:Cross-references: EMBL:Z74745; NID:g1419764; PID:e251831; PID:g1419765; MIPS:YOL003c  
A:Experimental source: strain S288C  
R:Hughes, B.; Pohl, T.M.  
submitted to the Protein Sequence Database, July 1996  
A:Reference number: S66885  
A:Accession: S66885  
A:Molecule type: DNA  
A:Residues: 1-378 <HUG>  
A:Cross-references: EMBL:Z74745; NID:g1419764; PID:e251831; PID:g1419765; MIPS:YOL003c

A:Experimental source: strain S288C  
R:Starky, F.; Holmberg, A.; Petersson, B.; Uhlen, M.  
Yeast 12, 1091-1095, 1996  
A:Title: The sequence of a 30 kb fragment on the left arm of chromosome XV from Sacch  
A:Reference number: S72130; MUID:97051599; PMID:8896276  
A:Accession: S72130  
A:Status: nucleic acid sequence not shown; translation not shown  
A:Molecule type: DNA  
A:Residues: 1-378 <STW>  
A:Cross-references: EMBL:U43491; NID:g1150992; PIDN:AAC49477.1; PID:g1150993  
A:Note: the nucleotide sequence was submitted to the EMBL Data Library, December 1995  
C:Genetics:  
A:Cross-references: SGD:S0005363  
A:Map position: 15L  
A:Note: YOL003c  
C:Keywords: transmembrane protein  
F:10-26/Domain: transmembrane #status predicted <TM1>  
F:124-140/Domain: transmembrane #status predicted <TM2>  
F:173-189/Domain: transmembrane #status predicted <TM3>  
Query Match 8.0%; Score 80; DB 2; Length 378;  
Best Local Similarity 23.7%; Pred. No. 8.1;  
Matches 41; Conservative 24; Mismatches 54; Indels 54; Gaps 9;  
QY 3 NRPSPKAPRASQMTFFFLFPSPF-----TGVLCTAI--TIWRKPSADCG 50  
Db 68 NYKPPDIDWRN-----FCKKQSYKPERSHCKTCNQCVMMDHCPWTM---NCV 115  
QY 51 PFRGLFLFHSIYSWIDLTST-----RPGYLVWYIRNLIG-----SVHP 91  
Db 116 GFANYPHFLEFLFWIITVTSVLFQIAKRIYFMOORHLPGYFFKSELFIETLSSPLNS 175  
QY 92 FFILITLIVLITLYLWQITEGRK----IMIRLHEQIINEGDKMFLIELI 139  
Db 176 FVLLITLITLFLRCLFNQILNGRSQIESWMDRL--ESLFNSGR----LQKLI 222  
RESULT 12  
B26696  
hypothetical protein 1 (CYB-COI1 intergenic region) - Leishmania tarentolae mitochond  
C:Species: mitochondrion Leishmania tarentolae  
C:Date: 31-Dec-1989 #sequence\_revision 31-Dec-1989 #text\_change 07-Dec-1999  
C:Accession: B26696  
R:Simpson, L.; Neckelmann, N.; de la Cruz, V.F.; Simpson, A.M.; Feagin, J.E.; Jansner,  
J. Biol. Chem. 262, 6182-6196, 1987  
A:Title: Comparison of the maxicircle (mitochondrial) genomes of Leishmania tarentola  
A:Reference number: A92643; MUID:87194837; PMID:3032958  
A:Accession: B26696  
A:Molecule type: DNA  
A:Residues: 1-443 <SIM>  
A:Cross-references: GB:M10126; GB:J02707; GB:M10127; GB:M1022; GB:M64690; GB:N00030;  
A:Note: the authors translated the codon ATT for residue 388 as Phe and TTC for resid  
C:Genetics:  
A:Genome: mitochondrion  
A:Genetic code: S66  
C:Superfamily: hypothetical protein 1 (CYB-COI1 intergenic region)  
C:Keywords: mitochondrion  
Query Match 8.0%; Score 80; DB 2; Length 443;  
Best Local Similarity 26.4%; Pred. No. 9.6;  
Matches 28; Conservative 21; Mismatches 35; Indels 22; Gaps 4;  
QY 20 FFLLFFPSFTGVLCTAIITWRKPSADCGPRGLFHSIYSWIDLTSTPRGYLVV 79  
Db 161 FCFLLRDEMLGILGCFYIILIFK-----LYIALILFLDQYIRLVGF--I 206  
QY 80 WYIRNLGSGVHFFFLITLVLIITLYLWQITEGRKIMIRLHEQII 135  
Db 207 FLY---MLTFYVLFCEFLIILILCFIFYI-----IFIKLIITQSI 244  
RESULT 13  
AD1305



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